Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-22. (Cancelled)

23. (Currently amended) A method of diagnosis, the method comprising:

(a) providing a test cell; [[and]]

(b) determining, in the test cell, the degree of methylation of one or more C residues in a nucleotide sequence in a genomic segment, the genomic segment consisting of (i) a CpG island in the HIN-1 5' promoter region and (ii) the first twelve nucleotides of SEQ ID NO:3, wherein the one or more C residues are C residues in CpG sequences[[,]]; and

(c) comparing the degree of methylation of the one or more C residues to the degree of methylation of corresponding one or more C residues in a corresponding genomic segment in a control cell, wherein a [[high]] higher degree of methylation of the one or more C residues in the test cell than in the control cell is an indication that the test cell is a cancer cell.

24. (Original) The method of claim 23, wherein the test cell is a breast cell.

25. (Withdrawn) An isolated polypeptide comprising (a) a functional fragment of the polypeptide of claim 8; or (b) the functional fragment, except for one or more conservative amino acid substitutions.

26. (Withdrawn) An isolated DNA comprising a fragment of the nucleic acid with SEQ ID NO:3, wherein the fragment comprises nucleotides 55 and 56 of SEQ ID NO:3.

27. (Withdrawn) An antibody that binds to the polypeptide of claim 8.

28. (Withdrawn) The antibody of claim 27, wherein the antibody is a monoclonal antibody.

29. (Withdrawn) The antibody of claim 27, wherein the antibody is a polyclonal antibody.

30. (Withdrawn) A method of treatment comprising

identifying a patient as having cancer cells in which (a) HIN-1 gene expression is low or (b) a HIN-1 promoter region is methylated; and

treating the patient with a compound that reduces methylation of the HIN-1 promoter region.

31. (Withdrawn) A method of identifying a compound that replaces the function of HIN-1 in cells that do not express HIN-1, the method comprising:

(a) providing a first cell that does not express HIN-1;

(b) providing a second cell that does express HIN-1;

(c) treating the first cell and the second cell with a test compound; and

(d) determining whether the test compound decreases proliferation of the first or the second cell, wherein a compound that decreases proliferation of the first cell but not the second cell can potentially replace the function of HIN-1 in cells that do not express HIN -1.

32. (Withdrawn) A method of treatment comprising

identifying a patient as having cancer cells in which (a) HIN-1 gene expression is low or (b) a HIN-1 promoter region is methylated; and

treating the patient with a compound that induces expression of a gene with a methylated promoter region.

33. (Withdrawn) The method of claim 23, wherein the cell is a pancreatic cell.

34. (Withdrawn) The method of claim 23, wherein the cell is a prostate cell.

35. (Previously presented) The method of claim 23, wherein the test cell is selected from the group consisting of a lung cell, a prostate cell, a pancreatic cell, a gastrointestinal cell, and a skin cell.

36. (Previously presented) The method of claim 23, wherein the promoter region comprises SEQ ID NO:19.

37. (Currently amended) The method of claim 36, wherein the promoter region consists of SEQ ID NO:19.

38. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ comprises nucleotide 1 to nucleotide 252 of SEQ ID NO:19.

39. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ consists of nucleotide 1 to nucleotide 252 of SEQ ID NO:19.

40. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ comprises nucleotide 229 to nucleotide 551 of SEQ ID NO:19 and nucleotide 1 to nucleotide 12 of SEQ ID NO:3.

41. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ consists of nucleotide 229 to nucleotide 551 of SEQ ID NO:19 and nucleotide 1 to nucleotide 12 of SEQ ID NO:3.

42. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ comprises SEQ ID NO:19 and nucleotide 1 to nucleotide 12 of SEQ ID NO:3.

43. (Currently amended) The method of claim 23, wherein the nucleotide sequence ~~segment~~ consists of SEQ ID NO:19 and nucleotide 1 to nucleotide 12 of SEQ ID NO:3.

44. (Previously presented) The method of claim 23, wherein the test cell is a human cell.

45. (Currently amended) The method of claim 23, wherein the degree of methylation is determined by sequencing of bisulfite-treated DNA comprising the ~~segment~~ nucleotide sequence.

46. (Previously presented) The method of claim 23, wherein the degree of methylation is determined by a methylation-specific polymerase chain reaction (MCP) assay.